```
StuAP           MASMNQPQPYMDVHS-HLSSGQTYASHPATAGALTHYQYPQQPPVLQP-TSTYGPASS-Y 57
SnStuA          ---MNQMQSYADVHPPHMSAATAHAPASAAPSGISHYAYPPQSSMMQPGQHQYGPTPPGY 57
FoStuA          ---MNQGHPQPDMYY------------------SPHYSTPQYG---------YGYSTNGA 30
                   *** :.  *::                    .**  *            ** :.

StuAP           SQYPYPNSVASSQSVPPPTTSISSQVPAQLLPLPVTNHPVPTHGYGNNSGTPMQGYVYDP 117
SnStuA          PSYGYSNGVPSG---LPASSSMNNAMVPSTLQLPAMSSSGPSPSLSG--AQSYAPHSFDH 112
FoStuA          PTTAVSTPMPAPQNVLPVPSALSNQGAMQQPGYSNSSNNG----------------AFDT 74
                .    .. :.:     * .:::..    .    .  .                    :*

StuAP           TGQMAPPGAKPRVTATLWEDEGSLCYQVEAKGVCVARREDNGMINGTKLLNVAGMTRGRR 177
SnStuA          TGQVAPPGMKPRVTATLWEDEGSLCFQVEAKGVCVARREDNHMINGTKLLNVAGMTRGRR 172
FoStuA          TGQHNPPGMKPRVTATLWEDEGSLCFQVEARGICVARREDNHMINGTKLLNVAGMTRGRR 134
                ***  *** ****************:****:*:******** ******************
                                                         APSES domain

StuAP           DGILKSEKVRNVVKIGPMHLKGVWIPFDRALEFANKEKITDLLYPLFVQHISNLLYHPAN 237
SnStuA          DGILKSEKTRHVVKIGPMHLKGVWIPFERALEFANKEKITEQLYPLFVHDIGALLYHPSN 232
FoStuA          DGILKSEKVRHVVKIGPMHLKGVWIPYDRALDFANKEKITELLFPLFVHNIGALLYHPSN 194
                ********.*:***************::***:********: *:****:.*. *****:*

StuAP           QNQR-----NMTVPDSRRLE--GPQPVVRTPQAQQPPSLHHH-SLQTPVPSHMSQP---- 285
SnStuA          QTRASVGSAAMAAVDRRRPDSMQTQRYISGPTTSQPPSLHHHHSMSNPIGAPMSQAPHAL 292
FoStuA          SNRTS---QVMAAAERRKHEGLGGQRPAAP---NALPSIGQHHPMMPGLPTGGYVP---- 244
                ..:       *:. : *: :    *        .  **: :* .:   : :    .

StuAP           -----GGRPSLDRAHTFPTPPASASSVP--------------------NTQPLSIDTSLS 320
SnStuA          QPHPSAGRPGLDRAHTFPTPPTSASSIMGMSNSGSSYEWSGANVQTPQGSQPLSIDTGLS 352
FoStuA          --------------QSLANGPQSLASTP-------------------------------- 258
                              :::.. * * :*

StuAP           NARSMPTTPATTPPGNNLQGMQSYQPQSGYD-SKPYYSAAPSTHPQYAPQQPLPQQSMAQ 379
SnStuA          NTRSVPTTPATTPPG-AVQQAISYGSNQSYDNSRPMYSGPPSQPGQYNTQG----QSMMG 407
FoStuA          ----QPLTNGSQPPMPNGGGMLKRGREEEEDLHRPVSNGHDPMSNMHAMSNGYPQQPPLA 314
                     * * .: **        .   :.  *  :*  ..  .    :  .     *.

StuAP           YGHSMPTSSYRDMAPPSSQRGSVTEIESDVKTER----YGQGTVAKTEP------EQEQE 429
SnStuA          YRPDS-GYTKTEMAPPS-RLADVSE-EGDVKHSEGMMPQGNSQVVAPAPGPEGDHEHDNE 464
FoStuA          NVHQPPMQNGGDMLKRGRDEDDEVHRSAHTAHDT------MNNMPGSMPGLSNAYAQPLP 368
                   .    .  :*   .    .  . ....  .        . :  . *       :

StuAP           YAQPDSGYNTGRGSY-YTTNPSVGGLAHDHSQLTPDMTGSPQQNGSGRMTPRTSNTAP-Q 487
SnStuA          YTHSTASYNGSRGPYGYASNGNAGGLHPEHPHMSPEMNGSPHQNGSGRATPRTTTTSQTQ 524
FoStuA          NVHHQPLANGDGGMLKRGRDEDDD--VHRSSPNGHDSAGNFEVKRRKTITSNDSMVSPGG 426
                 .:  .  * . *      : . .      .    :  *. . :     *.. : .:

StuAP           WAPGYTTPPRPAAASS--LYNIVSDTRGTSGANGSTSDNYSVASNSGYS-TGMNGSMGSN 544
SnStuA          WNSGYPTPQRQGPPSSN-LYNVMSDPRGAPNGNAPHDAYPGPGAVPQYASQGYPPANGNA 583
FoStuA          FYTLHNGYGQPGVMNGMSPYKRRDDEAETPRPGPNVHDHLNNFDLKRHKTMETSVPAPQY 486
                : . :    : .  ..   *:  .*   :.  .       .      :       .  .

StuAP           KRMRDDDDDRIVPPDSRGEFDT---KRRKTLTETPVGGPVGGVP-LGLQQ---------- 590
SnStuA          KRGRDDDDEDPYRPDSVQSDDMGGLKRRKTMEGGAVGGAYAQDPTPGLQRAHTMTAQRAR 643
FoStuA          DAMNRPHSSIGTSPTYAPAPVYDNLARPASTVAASPSYPSAPVYDTGARPPSAISAPRRQ 546
                .  .  ...    *            *  :    . . . .     *  :

StuAP           ----
SnStuA          R--- 644
FoStuA          QSFG 550
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Fig. S1. Multiple sequence alignment of SnStuA (SNOG_14941) against StuAp (XP_663440) from *A. nidulans* and FoStuA (BAD21357) from *F. oxysporum* using EBI Clustalw. The bold and italicized sequences show the APSES domain.